

109070" Z200660

FIGURE 1

SEQ ID NO:26	AREANAGLVAGSYKRNELVIRIHRDSDGQOPKEANGQICQICGDTVGKSGATGDTFVAC	**** *	*** ** *
SEQ ID NO:30	-----MDGADAL-KSGRHGAGVQCICADGLGTTLDGDFVAC		
SEQ ID NO:33	-----MESEGETAGPKMKNIVPQTQCICSDNVGKTVDGDRFVAC		
	1		60
SEQ ID NO:26	NECGFPVCRPCYEYERKDGNCQCCPOCKTRYKRQKGSPRVEGDEEEDVDLLEN-EFNYSG	*****	***
SEQ ID NO:30	DVCRFPVCRPCYEYERKEGTQACLOCKTKYKRHRGSPAIRGEGDDTDADGGS-DFN1PA		
SEQ ID NO:33	DICSFVCRPCYEYERKDGNCQCCPOCKTRYKRRLKGSPIFGDKDEGLADEGTVFENYP-		
	61		120
SEQ ID NO:26	KGKNQK--KVTTRARPWQ---GDOQDIELS-----VSSSRHDESQOP---VPLLTHGHS	* * *	* * *
SEQ ID NO:30	SGTEQKQKIADRMRSWRMNTGGSGNVGHPKYDSGEI GLSKYDSGEIPRGYVFSVTSNQ-		
SEQ ID NO:33	-----QKEKISERMLGWHLTRKGGEEMPQYDK-----EVSHNHLPRLTSRQD		
	121		180
SEQ ID NO:26	VSGEIPTPDNHSIRTTSGPIGPVEKSIPIYIDPROPAVRILIVDPFSKDLNSYGLGNVDMKE	***	***
SEQ ID NO:30	MSGEIPGASPD--HHMSPGTGNISRRAPFY-VNHSNPSREFSG-----SIGNVAWKE		
SEQ ID NO:33	TSGEFSAASPE--RLSVSSTIAGGKRLFPSSDVNQSPNRRIVDPV-----GLGNVAWKE		
	181		240
SEQ ID NO:26	RVEGWKLKQEKNNVQMTS-----RYPEGKDGTEGTGNSG--EELQMAADDIROPMRSRIPI	*** ** *	*** ** *
SEQ ID NO:30	RVDGWMKQDKGAIPMTNGTSTIAPESGAAATDIDASTEYNMEDALLINDETROPLSRKYPVI		
SEQ ID NO:33	RVDGWMKQEKNTGPV-----STQAAASERGGVDIDASTDILADEALLINDEARQPLSRKYSI		
	241		300

FIGURE 1 CONTINUED

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SEQ ID NO:26      ****          *****          *****          *****          *****
SEQ ID NO:30      NNSCLKAMCFMNDPNLGGKTCYQVQRFQDGDILHRYANRNIVFFDINLKGLDGQIG
SEQ ID NO:33      NNSKAVREAMCFMNDPNLGPQVCYQVQRFQDGDILHRYANRNIVFFDINLRLGLDQIG
601              NNSKALREAMCFMNDPNLKGQVCYQVQRFQDGDILHRYANRNIVFFDINLRLGLDQIG
              660

SEQ ID NO:26      *****          ***          *          *          *          *
SEQ ID NO:30      PVYVGTCCCFNRQALYDPLVTEEDLEPNIIKSCGSRKKKGKGNKKYIDKNRALKRT
SEQ ID NO:33      PVYVGTGCVFNRTAIYGEPPIAK--RPGELASLCGGKKKASKS-KKRSSDKKKSNKHV
661              PVYVGTGCVFNRTALYGEPPIAKVKHKKPSLLSKLGGSRKKNSK-AKESDKKKSGRHT
              720

SEQ ID NO:26      *          *          *****          *          *          *          *
SEQ ID NO:30      ESTAPIENMEDIEEGIE--GYDDERSFLMAQ-SYEKRFGQSPVLIATFMEQGGLPSTN
SEQ ID NO:33      DSSVPVFENLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFQSAFVASTLMYEGVQGST
721              DSTVPVFNLDIEEGVEGAGFDDEKALLMSQMSLEKRFQSAFVASTLMENGVPVPSAT
              780

SEQ ID NO:26      *****          **          *****          ***          *          *          *
SEQ ID NO:30      SATLLKEAIHVI SCGYEDKTEWGKEIGWIYGSVTEIDILTGFKMHTRGWISYICMPRPAP
SEQ ID NO:33      PESLLKEAIHVI SCGYEDKSEWGTGIGWIYGSVTEIDILTGFKMHARGWRSYICMPKRPAP
781              PENLLKEAIHVI SCGYEDKSDWGMGIEIGWIYGSVTEIDILTGFKMHARGWRSYICMPKLPAP
              840

SEQ ID NO:26      *****          ***          *****          *          *          *          *
SEQ ID NO:30      KGSAPINLSDRLNQVLRWALGSVEILFSRHCPIMWYSGRLKFLERLAYINTIYVPLTSL
SEQ ID NO:33      KGSAPINLSDRLNQVLRWALGSVEILFSRHCPIMWYSGRLKFLERLAYINTIYVPLTSL
841              KGSAPINLSDRLNQVLRWALGSVEILFSRHCPIMWYSGRLKFLERLAYINTIYVPLTSL
              900

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FIGURE 1 CONTINUED

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PLLAYCTUPAICLLTGKFIPEISNYASIWIFILLFVSIFSTGILELRWSGVTLDEWWRNE
PLLVYCIILPAICLLTGKFIPEISNLASIWIFALSIFATGILEMRWSGVGIDEWWRNE
PLLMYCTLLAVCLFTNQFIIPQISNIASIWIFLSIFATGILEMRWSGVGIDEWWRNE
901
*****
QFWVIGGSAHLFAVFQGLLKVLGIDNFTVTSKASDEGDFAELYVFKWTSLLIPPTT
QFWVIGGSAHLFAVFQGLLKVLGIDNFTVTSKANDEEGDFAELYMFKWTTLLIPPTT
QFWVIGGSAHLFAVFQGLLKVLGIDNFTVTSKASDEGDFAELYLFKWTTLLIPPTT
961
*****
* * * * * * * * * * * * * * * * * * * * * * * * * * * *
ILVVMVGIVAGVSFAINSGYQSWGPLEFGRLEFAFWIVHLYPFLKGLLGRQNRPTTIV
ILIIINMVGIVAGTSYAINSGYQSWGPLEFGKLFFAFWIVHLYPFLKGLMGRQNRPTTIV
LLIVNLGVVAGVSYAINSGYQSWGPLEFGKLFFAFWIVHLYPFLKGLMGRQNRPTTIV
1021
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VMSVLIASIFSLWVRIDPFTSDSTKAR-GQCGIDC
VWAVLIASIFSLWVRIDPFTTRLAGPNIQTGGINC
VMSVLIASIFSLWVRIDPFTSRVTGPDIIECGINC
1081

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